

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i i i) NUMBER OF SEQUENCES: 33

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATTTAGCAGC ATTCCAGATT GGGTCAATC AACAAAGTAC GAGCCATATC ACTTTATTCA	60
AATTGOTATC GCCAAAAACCA AGAAGGAACT CCCATCCTCA AAAGTTTGTA AOGAAGAATT	120
CTCAGTCAA AGCCTCAACA AGGTCAAGGT ACAGAGTCTC CAAACCATTA GCCAAAAAGCT	180
ACAGGAGATC AATGAAGAAT CTTCAATCAA AGTAAACTAC TOTTCAGCA CATGATCAT	240
GOTCAAGTAAG TTTCAAGAAA AGACATCCAC CGAAGACTTA AAOTTAAGTGG GCATCTTGA	300
AAGTAATCTT GTCAACATCG AGCAOCTGOC TTGTOGGGAC CAGACAAAAA AGGAATGGTG	360
CAOAATTGTT AGGCOCACCT ACCAAAAAGCA TCTTTGCCTT TATTGCAAAA GATAAAAGCAG	420

-continued

ATTCCTCTAG TACAAGTGGG GAAACAAAATA ACGTGGAAAA GAGCTGTCCCT GACAGCCCAC	480
TCACTAATGC GTATGACGAA CGCAGTGACG ACCACAAAAAG AATTTTCCCT CTATATAAGA	540
AGGCATTTCA TTCCCATTG AAGG	564

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATCATCAGAT ACTAAACCAAT ATTTCCTC	27
---------------------------------	----

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1692 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:3:

NCATGGACGT CTGATCGAAA TCGTCOTTAC CGCACGCAAGG TAAGGCACGCC CGAATTITAT	60
CACCTACCGC GAAACGGTGG CTAGGCAOOG AGAGACTGTC GGCTCCGCCG GAGCATCCTA	120
TGTCTGAGAA CCACAAAAAA GTAGGCATCG CTGGAGGCCG AAATCGTCGG GTATGACCGG	180
CGCTGATGCT TCAGCGCCGC GGATTCAAAAG TCACCTTGAT TGACCCGAAC CCTCCCTGGCG	240
AAAGGTGCATC GTTTGGGAAT GCGGATGCT TCAACGGCTC ATCCGTCGTC CCTATGTCGA	300
TGCCGGGAAA CTTGACGAGC GTGCCGAAGT GGCTCCCTGA CCCGATGGGG CGGTTGTCAA	360
TCCGGTTCAAG CTATTTCCA ACCATCATGC CCTGGTTGAT TCGTTTCTG TTAGCCGGAA	420
GACCAAAACAA GGTGAAGGAG CAGGCAGAAAG CACTCCGCAA TCTCATCAAG TCCACGGTGC	480
CTCTGATCAA GTCATTGGCG GAGGAGGCTG ATCGAGGCCA TCTGATCCGC CATGGAAAGTC	540
ATCTGACCGT ATATCGTGA GAAGCAGACT TCGCCAAGGA CGCGGGAGGT TGGGAACTGC	600
GGCGTCTCAA CGGTGTTCGC ACGCAGATCC TCAOCCGCCG TGCGTTGCCG GATTTCGATC	660
CGAACTTGTGTC GCATGCOTTT ACCAAGGGCA TTCTTATAGA AGAGAACGGT CACACGATTA	720
ATCCGCAAGG GCTCGTGACC CTCTGTTTC GGCGTTTTAT CGCGAACGGT GGCGAACATCG	780
TATCTGCGCG TGTGATCGGC TTTGAGACTG AAAGTGGGGC GCTTAAAGGC ATTACAACCA	840
CGAACGGCGT TCTGGCCGTT GATOCAGCGG TTGTCGCAOC CGCGCGCACAC TCGAAATCAC	900
TTGCTAATTC GCTAGGCAT GACATCCCGC TCGATACCGA ACGTGGATAT CATATCGTCA	960
TCCGCGAATCC GGAAGCCGCT CCACGCATTC CGACGACCGA TCGTCAGGA AAATTCATCG	1020
CGACACCTAT GGAATGGGG CTTCGCOTGG CGGGTACGGT TGAAGTTCGCT GGGCTCACAG	1080
CCGCTCTAA CTGGAAACGGT CGCGATGTC TCTATACGCA CGCTCGAAAAA CCTCTTCCAG	1140
CCCTCOCGCC TOCGAGTTCT GAAGAACGAT ATTCCAAATG GATGGGGTTC CGGCCGAGCA	1200
TCCCGGATTC GCTCCCCGTC ATTGGCCGGG CAACCCGGAC ACCCGACGTA ATCTATGCTT	1260
TCCGCCATGG TCATCTCGC ATGACAGGGG CGCCGATGAC CGCAACGCTC GTCTCAGAGC	1320
TCCCTCGCAGG CGAAAAGACC TCAATCGACA TTTCGCCCTT CGCACCAAAC CGCTTGGTA	1380

-continued

TTGGCAAATC	CAAGCAAACG	GGTCCCGCAA	GTTAAGTACT	TACGCGOTCG	TGAGTACAGC	1440
GCAGAGCCGG	TGTCAAGATC	AATCTGCACC	TCGCAATCAC	CTCGGAGACG	CGAAATGGCG	1500
CAAATAGAAC	ACATATTAAC	GAGTCACGCC	CCGAAGCCTT	GGGGTCACTA	CAGTCAGGCC	1560
CCCCGAGCGG	GTGATTTCAT	TCATGTTTCC	GGTCAGCTTC	CGATCAAACC	AGAAGGCCAO	1620
TCGGAGCAAT	CTGACGATCT	CGTCGATAAC	CAAGCCAGTC	TCGTTCTCCG	GAATTTGCTG	1680
GGCGTACTCG	AG					1692

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATG	TCT	GAG	AAC	CAC	AAA	AAA	GTA	GGC	ATC	GCT	GGA	GCC	GGA	ATC	GTC	48
Met	Ser	Glu	Asn	His	Lys	Lys	Val	Gly	Ile	Ala	Gly	Ala	Gly	Ile	Val	
1		5					10							15		
GCG	GTA	TGC	ACG	GCG	CTG	ATG	CTT	CAG	CGC	CGC	GGA	TTC	AAA	GTC	ACC	96
Gly	Val	Cys	Tbr	Ala	Leu	Met	Leu	Gly	Arg	Arg	Gly	Phe	Lys	Val	Thr	
		20					25							30		
TTG	ATT	GAC	CCG	AAC	CCT	CCT	GGC	GAA	GGT	GCA	TCG	TTT	GGG	AAT	GCC	144
Leu	Ile	Asp	Pro	Asn	Pro	Pro	Gly	Glu	Gly	Ala	Ser	Phe	Gly	Asn	Ala	
	35					40						45				
GGA	TGC	TTC	AAC	GGC	TCA	TCC	GTC	GTC	CCT	ATG	TCC	ATG	CCG	GGA	AAC	192
Gly	Cys	Phe	Asn	Gly	Ser	Ser	Val	Val	Pro	Met	Ser	Met	Pro	Gly	Asn	
	50					55						60				
TTG	ACG	AGC	GTC	CCG	AAG	TGG	CTC	CTT	GAC	CCG	ATG	GGC	CGT	TGT	CAA	240
Leu	Tbr	Ser	Val	Pro	Lys	Trp	Leu	Leu	Asp	Pro	Met	Gly	Arg	Cys	Gly	
	65				70			75						80		
TCC	GGT	TCA	GCT	ATT	TCC	AAC	CAT	CAT	GCC	TGG	TTG	ATT	CGC	TTT	CTG	288
Ser	Gly	Ser	Ala	Ile	Ser	Asn	His	His	Ala	Trp	Leu	Ile	Arg	Phe	Leu	
	85					90						95				
TTA	GCC	GGG	AGA	CCA	AAC	AAG	GTG	AAG	GAG	CAG	GCG	AAA	GCA	CTC	CGC	336
Leu	Ala	Gly	Arg	Pro	Asn	Lys	Val	Lys	Gly	Gly	Ala	Lys	Ala	Leu	Arg	
	100					105						110				
AAT	CTC	ATC	AAG	TCC	ACG	GTG	CCT	CTG	ATC	AAG	TCA	TTG	GCG	GAG	GAG	384
Asn	Leu	Ile	Lys	Ser	Tbr	Val	Pro	Leu	Ile	Lys	Ser	Leu	Ala	Glu	Gly	
	115					120						125				
GCT	GAT	GCG	AGC	CAT	CTG	ATC	CGC	CAT	GAA	GGT	CAT	CTG	ACC	GTA	TAT	432
Ala	Asp	Ala	Ser	His	Leu	Ile	Arg	His	Glu	Gly	His	Leu	Tbr	Val	Tys	
	130					135						140				
CGT	GGA	GAA	GCA	GAC	TTC	GCC	AAG	GAC	CGC	GGA	GOT	TGG	GAA	CTG	CGG	480
Arg	Gly	Glu	Ala	Asp	Phe	Ala	Lys	Asp	Arg	Gly	Gly	Trp	Glu	Leu	Arg	
	145					150						155			160	
CGT	CTC	AAC	GGT	GTT	CGC	ACG	CAG	ATC	CTC	AGC	GCC	GAT	GCG	TTG	CGG	528
Arg	Leu	Asn	Gly	Val	Arg	Tbr	Gly	Ile	Leu	Ser	Ala	Asp	Ala	Leu	Arg	
	165						170						175			
GAT	TTC	GAT	CCG	AAC	TTC	TCG	CAT	GCG	TTT	ACC	AAG	GCG	ATT	CIT	ATA	576
Asp	Phe	Asp	Pro	Asn	Leu	Ser	His	Ala	Phe	Tbr	Lys	Gly	Ile	Leu	Ile	
	180					185						190				
GAA	GAG	AAC	GGT	CAC	ACG	ATT	AAT	CCG	CAA	GGG	CTC	GTG	ACC	CTC	TTG	624
Gly	Gly	Asn	Gly	His	Tbr	Ile	Asn	Pro	Gly	Gly	Leu	Val	Tbr	Leu	Leu	

-continued

195	200	205	
TTT CGG CGT TTT ATC GCG AAC GGT GGC GAA TTC GTA TCT GCG CGT GTC Phe Arg Arg Phe Ile Ala Asn Gly Gly Glu Phe Val Ser Ala Arg Val 210 215 220			672
ATC GGC TTT GAG ACT GAA GGT AGG GCG CTT AAA GGC ATT ACA ACC ACG Ile Gly Phe Glu Thr Glu Gly Arg Ala Leu Lys Gly Ile Thr Thr Thr 225 230 235 240			720
AAC GGC GTT CTG GCC GTT GAT GCA GCG GTT GTC GCA GCC GGC GCA CAC Asn Gly Val Leu Ala Val Asp Ala Ala Val Val Ala Ala Gly Ala His 245 250 255			768
TCG AAA TCA CTT GCT AAT TCG CTA GGC GAT GAC ATC CCG CTC GAT ACC Ser Lys Ser Leu Ala Asn Ser Leu Gly Asp Asp Ile Pro Leu Asp Thr 260 265 270			816
GAA CGT GGA TAT CAT ATC GTC ATC GCG AAT CCG GAA GCC GCT CCA CGC Glu Arg Gly Tyr His Ile Val Ile Ala Asn Pro Glu Ala Ala Pro Arg 275 280 285			864
ATT CCG ACG ACC GAT GCG TCA GGA AAA TTC ATC GCG ACA CCT ATG GAA Ile Pro Thr Thr Asp Ala Ser Gly Lys Phe Ile Ala Thr Pro Met Glu 290 295 300			912
ATG GGG CTT CGC GTG GCG GGT ACG GTT GAG TTC GCT GGG CTC ACA GCC Met Gly Leu Arg Val Ala Gly Thr Val Glu Phe Ala Gly Leu Thr Ala 305 310 315 320			960
GCT CCT AAC TGG AAA CGT GCG CAT GTG CTC TAT ACG CAC GCT CGA AAA Ala Pro Asn Trp Lys Arg Ala His Val Leu Tyr Thr His Ala Arg Lys 325 330 335			1008
CTT CTT CCA GCC CTC GCG CCT GCG AGT TCT GAA GAA CGA TAT TCC AAA Leu Leu Pro Ala Leu Ala Pro Ala Ser Ser Glu Glu Arg Tyr Ser Lys 340 345 350			1056
TGG ATG GGG TTC CCG CCG AGC ATC CCG GAT TCG CTC CCC GTG ATT GGC Trp Met Gly Phe Arg Pro Ser Ile Pro Asp Ser Leu Pro Val Ile Gly 355 360 365			1104
CGG GCA ACC CGG ACA CCC GAC GTA ATC TAT GCT TTC GGC CAT GGT CAT Arg Ala Thr Arg Thr Pro Asp Val Ile Tyr Ala Phe Gly His Gly His 370 375 380			1152
CTC GGC ATG ACA GGG GCG CCG ATG ACC GCA ACG CTC GTC TCA GAG CTC Leu Gly Met Thr Gly Ala Pro Met Thr Ala Thr Leu Val Ser Glu Leu 385 390 395 400			1200
CTC GCA GGC GAA AAG ACC TCA ATC GAC ATT TCG CCC TTC GCA CCA AAC Leu Ala Gly Glu Lys Thr Ser Ile Asp Ile Ser Pro Phe Ala Pro Asn 405 410 415			1248
CGC TTT GGT ATT GGC AAA TCC AAG CAA ACG GGT CCG GCA AGT TAA Arg Phe Gly Ile Gly Lys Ser Lys Glu Thr Gly Pro Ala Ser 420 425 430			1293

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 430 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ser Glu Asn His Lys Lys Val Gly Ile Ala Gly Ala Gly Ile Val 1 5 10 15
Gly Val Cys Thr Ala Leu Met Leu Glu Arg Arg Gly Phe Lys Val Thr 20 25 30
Leu Ile Asp Pro Asn Pro Pro Gly Glu Gly Ala Ser Phe Gly Asn Ala 35 40 45
Gly Cys Phe Asn Gly Ser Ser Val Val Pro Met Ser Met Pro Gly Asn

-continued

50	55	60
Leu	Thr	Ser
65	Val	Pro
	Pro	Lys
	Tyr	Leu
	Leu	Asp
		Pro
		Met
		Gly
		Arg
		Cys
		Gln
		80
Ser	Gly	Ser
85	Ala	Ile
	Ser	Asn
	His	His
	Ala	Tyr
	Leu	Ile
		Arg
		Phe
		Leu
		95
Leu	Ala	Gly
100		Arg
	Pro	Pro
	Asn	Lys
	Val	Val
		Lys
		Glu
		Gln
		Ala
		Lys
		Ala
		Leu
		Arg
		110
Asn	Leu	Ile
115		Lys
	Ser	Thr
	Val	Pro
	Leu	Ile
		Lys
		Ser
		Leu
		Ala
		Glu
		Glu
		125
Ala	Asp	Ala
130	Ser	His
	Leu	Ile
		Arg
		His
		Glu
		Gly
		His
		Leu
		Thr
		Val
		Tyr
		140
Arg	Gly	Glu
145	Ala	Asp
	Phe	Ala
	Lys	Asp
		Arg
		Gly
		Gly
		Trp
		Glu
		Leu
		Arg
		160
Arg	Leu	Asn
165	Gly	Val
	Arg	Thr
	Gln	Val
		Lys
		Ser
		Ala
		Asp
		Ala
		Leu
		Arg
		175
Asp	Phe	Asp
180	Pro	Asn
	Leu	Ser
		His
		Phe
		Thr
		Lys
		Gly
		Ile
		Leu
		Ile
		190
Glu	Glu	Asn
195	Gly	His
	Thr	Ile
	Asn	Pro
		Gln
		Gly
		Leu
		Val
		Thr
		Leu
		Leu
		205
Phe	Arg	Arg
210	Phe	Ile
	Ala	Asn
		Gly
		Gly
		Glu
		Phe
		Val
		Ser
		Ala
		Arg
		Val
		215
Ile	Gly	Phe
225	Glu	Thr
	Gly	Arg
	Ala	Leu
		Lys
		Gly
		Ile
		Thr
		Thr
		240
Asn	Gly	Val
245	Leu	Ala
	Val	Asp
	Ala	Ala
	Val	Val
	Ala	Ala
	Gly	Ala
		His
		255
Ser	Lys	Ser
260	Leu	Ala
	Asn	Ser
	Leu	Gly
		Asp
		Asp
		Ile
		Pro
		Leu
		Asp
		Thr
		270
Glu	Arg	Gly
275	Tyr	His
	Ile	Val
	Ile	Ala
	Asn	Pro
		Glu
		Ala
		Ala
		Pro
		Arg
		285
Ile	Pro	Thr
290	Thr	Asp
	Ala	Ser
		Gly
		Lys
		Phe
		Ile
		Ala
		Thr
		Pro
		Met
		Glu
		320
Met	Gly	Leu
305	Arg	Val
	Val	Ala
		Gly
		Thr
		Val
		Glu
		Phe
		Ala
		Gly
		Leu
		Thr
		Ala
		315
Ala	Pro	Asn
325	Trp	Lys
		Arg
		Ala
		His
		335
Leu	Leu	Pro
340	Ala	Leu
	Ala	Pro
	Ala	Ser
		Ser
		345
Trp	Met	Gly
355	Phe	Arg
	Pro	Pro
	Ser	Ile
	Pro	Asp
	Ser	Leu
	Pro	Val
		Ile
		Gly
		365
Arg	Ala	Tyr
370	Arg	Thr
	Pro	Asp
	Val	Ile
	Tyr	Ala
	Phe	Gly
	Gly	His
		380
Leu	Gly	Met
385	Thr	Gly
	Ala	Pro
	Met	Met
	Thr	Ala
	Leu	Val
	Val	Ser
		Glu
		Leu
		400
Leu	Ala	Gly
405	Gly	Lys
	Thr	Ser
	Ile	Asp
		Ile
		Ser
		410
Arg	Phe	Gly
420	Ile	Gly
	Lys	Ser
	Ser	Lys
		Gly
		Thr
		425
Arg	Phe	Gly
	Ile	Gly
	Lys	Ser
	Ser	Lys
		Gly
		Pro
		Ala
		Pro
		Asn
		430

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

-continued

(i i) MOLECULE TYPE: DNA (recombinant)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:6

ATGGCTGAGA	ACCACAAAAA	AGTAGGCATC	GCTGGAGCCG	GAATCGTCGG	CGTATGCACG	60
GCGCTGATGC	TTCAACGCG	CGGATTCAAA	GTCACCTTGA	TTGACCCGAA	CCCTCCTGGC	120
GAAGGTGCAT	CGTTTGGAA	TGCCGGATGC	TTCAACGGCT	CATCCGTCGT	CCCTATGTCC	180
ATGCCGGAA	ACTTGACGAG	CGTGCCGAAG	TGGCTCCCTG	ACCCGATGGG	GCCGTTGTCA	240
ATCCGGTTCA	GCTATTTCC	AACCATCATG	CCCTGGTTGA	TTCOCTTTCT	GTAGCCGGA	300
AGACCAAACA	AGGTOAAGGA	OCAGGCAGAA	GCACCTCCGCA	ATCTCATCAA	GTCCACCGTG	360
CCTCTGATCA	AGTCATTGGC	GGAGGAGGCT	GATGCGAGCC	ATCTGATCCG	CCATGAAGGT	420
CATCTGACCG	TATATCGTGG	AGAAGCAGAC	TTCCGCCAAGG	ACCGCGGAGG	TTGGGAACTG	480
CGCGTCTCA	ACGGTGTTCG	CACGCAGATC	CTCAGCGCCG	ATGCGTTGG	GGATTTCGAT	540
CCGAACTTGT	CGCATGCGTT	TACCAAGGGC	ATTCTTATAG	AAGAGAACGG	TCACACGATT	600
AATCCGCAAG	GGCTCGTGAC	CCTCTTGT	CGGCGTTTA	TCGCGAACGG	TGGCGAATT	660
GTATCTGCAC	GTGTCATCGG	CTTGAGACT	GAAGGTAGGG	CGCTTAAAGG	CATTACAACC	720
ACGAACGGCG	TTCTGGCCGT	TGATGCGAGC	GTTGTCGAG	CCGGCGCACA	CTCGAAATCA	780
CTTGCTAATT	CGCTAGGCAG	TGACATCCCG	CTCGATACCG	ACGCTGGATA	TCATATCGTC	840
ATCGCGAAC	CGGAAGCCGC	TCCACGCATT	CCGACGACCG	ATGCGTCAGG	AAAATTCA	900
CGCACACCTA	TGGAAATGGG	CGTTCCGCGT	CGGGGTACGG	TTGAGTTGCG	TGGGCTCACA	960
CCCGCTCCTA	ACTGGAAACG	TGCGCATGTG	CTCTATACGC	ACGCTCGAAA	ACTTCTTCCA	1020
CCCCTCGCGC	CTGCGAGTTC	TGAGAACGA	TATTCCAAT	GGATGGGTT	CCGGCCGAGC	1080
ATCCCAGGATT	CGCTCCCCGT	GATTGGCCGG	GCAACCCGGA	CACCCGACGT	AATCTATGCT	1140
TTCGGCCACG	GTCATCTCGG	CATGACAGGG	GCGCCGATGA	CCGCAACGCT	CGTCTCAGAG	1200
CTCCCTCGCAG	CGAAGAAAGAC	CTCAATCGAC	ATTCTGCCCT	TCGACCAAAA	CCGCTTTGGT	1260
ATTGGCAAAT	CCAAGCAAAAC	GGGTCCGGCA	AGTTAA			1296

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (recombinant)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGGCTGAGA	ACCACAAAAA	AGTAGGCATC	GCTGGAGCTG	GAATCGTGG	TGTATGCACT	60
GCTTGTGATGC	TTCAACGCTG	TGGATTCAAA	GTCACCTTGA	TTGACCCGAA	CCCTCCTGGC	120
GAAGGTGCAT	CGTTTGGAA	TGCCGGATGC	TTCAACGGCT	CATCCGTCGT	CCCTATGTCC	180
ATGCCGGAA	ACTTGACGAG	CGTCCCGAAG	TGGCTCCCTG	ACCCGATGGG	GCCGTTGTCA	240
ATCCGTTCA	GCTATTTCC	AACCATCATG	CCCTGGTTGA	TTCOCTTTCT	GTAGCCGGA	300
AGACCAAACA	AGGTOAAGGA	OCAGGCAGAA	GCACCTCCGCA	ATCTCATCAA	GTCCACCGTG	360
CCTCTGATCA	AGTCATTGGC	GGAGGAGGCT	GATGCGAGCC	ATCTGATCCG	CCATGAAGGT	420
CATCTGACCG	TATATCGTGG	AGAAGCAGAC	TTCCGCCAAGG	ACCGCGGAGG	TTGGGAACTG	480
CGCGTCTCA	ACGGTGTTCG	CACGCAGATC	CTCTCTGCTG	ATGCTTGG	TGATTTCGAT	540
CCTAACCTTGT	CGCATGCTT	TACCAAGGGC	ATTCTTATAG	AAGAGAACGG	TCACACGATT	600

-continued

AATCCGCAAG	GGCTCGTGAC	CCTCTTGT	CGCGTTTA	TCGCGAACGG	TGGCGAATT	660
GTATCTGC	CGTGCATCGG	TTTGAGACT	GAAGGTGCG	CTCTCAAAGG	CATTACAACC	720
ACTAACGGTG	TTCTGGCTGT	TGATGCAGCT	GTGTTGCAG	CTGGTGCACA	CTCTAAATCA	780
CTTGCTAATT	CGCTAGGC	TGACATCCC	CTCGATACCG	AACGTGGATA	TCATATCGIC	840
ATCGCGAAC	TCGAGCCGC	TCCACGCATT	CCGACGACCG	ATGCGTCAGG	AAAATTCA	900
GCGACACCTA	TGAAATGGG	TCTTCGTGTT	GCTGGTACTG	TTGAGTTGC	TGGTCTCACA	960
GCTGCTCTTA	ACTGGAAACG	TGCCCATG	CTCTATAACCG	ACGCTCGAAA	ACTTCTTCCA	1020
GCCCTCGCGC	CTGCGAGTTC	TGAAGAACGA	TATTCCAAAT	GGATGGGTTT	TCGTCCTAGC	1080
ATTCCTGATT	CTCTTCCAGT	GATTGGTCGT	GCAACTCGTA	CACCGACGT	AATCTATGCT	1140
TTTGGTCACG	GTCATCTCGG	TATGACAGGT	GCTCCAATGA	CTGCAACTCT	CGTCTCAGAG	1200
CTCCTCGCAG	GCGAAAAGAC	CTCAATCGAC	ATTCGCCCT	TCGCACCAAA	CCGCTTTGGT	1260
ATTGGCAAAT	CCAAGCAAAAC	GGGTCCGGCA	AGTTAA			1296

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGGCTGAGA	ACCACAAGAA	GGTTGGTATC	GCTGGAGCTG	GAATCGTTGG	TGTTTGCACT	60
GCTTTGATGC	TTCAACGTCG	TGATTCAAG	GTACCTTGA	TTGATCCAAA	CCCACCAAGT	120
GAAGGTGCTT	CTTTCGGTAA	CGCTGGTGC	TTCAACGGTT	CCTCCGTTGT	TCCAATGTCC	180
ATGCCAGGAA	ACTTGACTAG	CGTTCCAAAG	TOGTTCTTG	ACCCAATGGG	TCCATTGTCC	240
ATCCGTTCA	GCTACTTCC	AACCATCATG	CCTTGGTTGA	TTCGTTCTT	GCTTGCTGGA	300
AGACCAAACA	AGGTGAAGGA	GCAAGCTAAG	GCACCTCGTA	ACCTCATCAA	GTCCACTGTG	360
CCTTTOATCA	AGTCCTTGCG	TGAGGAGGT	GATGCTAGCC	ACCTTATCCG	TCACGAAGGT	420
CACCTTACCG	TGTACCGTGG	AGAAGCAGAC	TTCGCCAAGG	ACCGTGGAGG	TTGGGAACCT	480
CGTCGCTCTA	ACGGTGTTCG	TACTCAAATC	CTCAGCGCTG	ATGCATTGCG	TGATTTCGAT	540
CCTAACTTGT	CTCACGCC	TACCAAGGG	ATCCTTATCG	AAGAGAACGG	TCACACCATC	600
AACCCACAAG	GTCTCGTGAC	TCTCTTGT	CGTCGTTCA	TCGCTAACGG	TGGAGAGTTC	660
GTGTCTOCTC	GTGTTATCGG	ATTGAGACT	GAAGGTGCG	CTCTCAAGGG	TATCACCACC	720
ACCAACGGTG	TTCTTGCTGT	TGATGCAGCT	GTTGTTGCAG	CTGGTGCACA	CTCCAAGTCT	780
CTTGCTAACT	CCCTTGGTGA	TGACATCCC	TTGGATACCG	AACGTGGATA	CCACATCGTG	840
ATGCCCAACC	CAGAACGTC	TCCACGTATT	CCAACCTACCG	ATGTTCTGG	AAAGTTCATC	900
GCTACTCCTA	TGGAATGGG	TCTTCGTGTT	GCTGGAACCG	TTGAGTTGC	TGGTCTCACT	960
GCTGCTCCTA	ACTGAAAGCG	TGCTCACGTT	CTCTACACTC	ACGCTCGTAA	GTTGCTTCCA	1020
GCTCTCGCTC	CTGCCAGTTC	TGAAGAACGT	TACTCCAAGT	GGATGGGTTT	CCGTCACAGC	1080
ATCCCAGATT	CCCTTCCAGT	GATGAGTCGT	GCTACCCGTA	CTCCAGACGT	TATCTACGCT	1140
TTCGGTACG	GTCACCTCGG	TATGACTGTT	GCTCCAATGA	CCGCAACCC	CGTTTCTGAG	1200
CTCCTCGCAG	GTOAGGAAGAC	CTCTATCGAC	ATCTCTCCAT	TCGCACCAAA	CCGTTTCCGT	1260

-continued

ATGGTAAGT CCAAGCAAAAC TGGTCCTGCA TCCTAA

1296

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (recombinant)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGATCTCCAC AATGGCTTCC TCTATGCTCT CTTCCGCTAC TATGGTTGCC TCTCCGGCTC	60
AGGCCACTAT GGTCGCTCCT TTCAACCGAC TTAAGTCCTC CGCTGCCTTC CCAGCCACCC	120
GCAAGGCTAA CAACGACATT ACTTCCATCA CAAGCAACCG CGGAAGAGTT AAC TGCATGC	180
AGGTGTGGCC TCCGATTGGA AAGAAGAAGT TTGAGACTCT CTCTTACCTT CCTGACCTTA	240
CCGATTCGGG TGGTCGCGTC AACTGCATGC AGGCCATGG	279

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (recombinant)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGATCTATCG ATAAGCTTGA TGTAATTGGA GGAAGATCAA AATTTCAAT CCCCATTC	60
CGATTGCTTC ATTGAAGTT TCTCCGATGG CGCAAGTTAG CAGAATCTGC AATGGTGTGC	120
AGAACCCATC TCTTATCTCC AATCTCTCGA AATCCAGTCA ACGCAAATCT CCCTTATCGG	180
TTCTCTGAA GACGCAGCAG CATCCACGAG CTTATCCGAT TTCGTCGTG TGGGGATTGA	240
AGAAGAGTGG GATGACGTTA ATTGGCTCTG AGCTTCGTCC TCTTAAGGTC ATGTCTTCTG	300
TTTCCACGGC GTGCATGC	318

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:11:

NCATGGACGT CTGATCGAAA TCGTCGTTAC CGCAGCAAGG TAAGGCACGC CGAATTTAT	60
CACCTACCGC GAAACGGTGG CTAGGCAGCG AGAGACTGTC GGCTCCCGGG GAGCATCCT	119

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:12:

5,776,760

59

60

-continued

GTACTTACGC GGTCTGTAAGT ACAGCGCAGA GCGGGTGTCA AGATCAATCT GCACCTCGCA	60
ATCACCTCGG AGACGCGAAA TGGCGCAAAT AGAACACATA TTAACCGAGTC ACGCCCCGAA	120
GCTTTGGGT CACTACAGTC AGGCGGCCCCG AGCGGGTGGG TTCATTCACTG TTTCCGGTCA	180
GCTTCCGATC AAACCAGAAG GCCAGTCGGA GCAATCTGAC GATCTCGTCG ATAACCAGGC	240
CAGTCTCGTT CTCCGGAATT TGCTGGCCGT ACTCGAG	277

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGAGACTGT CGACTCCGCG GGAGCATCAT ATG	33
--------------------------------------	----

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAACGAAATCC AAGCTTCTCA CGACCGCGTA AGTAC	35
---	----

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCCGAGATGA CCGTGGCCGA AAGC	24
----------------------------	----

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGAAATGCCG GATGCTTCAA CGGC	24
----------------------------	----

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (recombinant)

-continued

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATG GCT GAG AAC CAC AAG AAG GTT GGT ATC GCT GGA GCT GGA ATC GTT	48
Met Ala Glu Asn His Lys Lys Val Gly Ile Ala Gly Ala Gly Ile Val	
1 5 10 15	
GGT GTT TGC ACT GCT TTG ATG CTT CAA CGT CGT GGA TTC AAG GTT ACC	96
Gly Val Cys Thr Ala Leu Met Leu Glu Arg Arg Gly Phe Lys Val Thr	
20 25 30	
TTG ATT GAT CCA AAC CCA CCA GGT GAA GGT GCC TCT TTC GGT AAC GCT	144
Leu Ile Asp Pro Asn Pro Pro Gly Glu Gly Ala Ser Phe Gly Asn Ala	
35 40 45	
GGT TGC TTC AAC GGT TCC TCC GTT GTT CCA ATG TCC ATG CCA GGA AAC	192
Gly Cys Phe Asn Gly Ser Ser Val Val Pro Met Ser Met Pro Gly Asn	
50 55 60	
TTG ACT AGC GTT CCA AAG TGG CTT CTT GAC CCA ATG GGT CCA TTG TCC	240
Leu Thr Ser Val Pro Lys Trp Leu Leu Asp Pro Met Gly Pro Leu Ser	
65 70 75 80	
ATC CGT TTC GGC TAC TTT CCA ACC ATC ATG CCT TGG TTG ATT CGT TTC	288
Ile Arg Phe Gly Tyr Phe Pro Thr Ile Met Pro Trp Leu Ile Arg Phe	
85 90 95	
TTG CTT GCT GGA AGA CCA AAC AAG GTG AAG GAG CAA GCT AAG GCA CTC	336
Leu Leu Ala Gly Arg Pro Asn Lys Val Lys Glu Glu Ala Lys Ala Leu	
100 105 110	
CCT AAC CTC ATC AAG TCC ACT GTG CCT TTG ATC AAG TCC TTG GCT GAG	384
Arg Asn Leu Ile Lys Ser Thr Val Pro Leu Ile Lys Ser Leu Ala Glu	
115 120 125	
GAG GCT GAT GCT AGC CAC CTT ATC CGT CAC GAA GGT CAC CTT ACC GTG	432
Glu Ala Asp Ala Ser His Leu Ile Arg His Glu Gly His Leu Thr Val	
130 135 140	
TAC CGT GGA GAA GCA GAC TTC GCC AGG GAC CGT GGA GGT TGG GAA CTT	480
Tyr Arg Gly Glu Ala Asp Phe Ala Arg Asp Arg Gly Gly Trp Glu Leu	
145 150 155 160	
CGT CGT CTC AAC GGT GTT CGT ACT CAA ATC CTC AGC GCT GAT GCA TTG	528
Arg Arg Leu Asn Gly Val Arg Thr Glu Ile Leu Ser Ala Asp Ala Leu	
165 170 175	
CGT GAT TTC GAT CCT AAC TTG TCT CAC GCC TTT ACC AAG GGA ATC CTT	576
Arg Asp Phe Asp Pro Asn Leu Ser His Ala Phe Thr Lys Gly Ile Leu	
180 185 190	
ATC GAA GAG AAC GGT CAC ACC ATC AAC CCA CAA GGT CTC GTG ACT CTC	624
Ile Glu Glu Asn Gly His Thr Ile Asn Pro Glu Gly Leu Val Thr Leu	
195 200 205	
TTG TTT CGT CGT TTC ATC OCT AAC GGT GGA GAG TTC GTG TCT GCT CGT	672
Leu Phe Arg Arg Phe Ile Ala Asn Gly Glu Phe Val Ser Ala Arg	
210 215 220	
GTG ATC GGA TTC GAG ACT GAA GGT CGT GCT CTC AAG GGT ATC ACC ACC	720
Val Ile Gly Phe Glu Thr Glu Gly Arg Ala Leu Lys Gly Ile Thr Thr	
225 230 235 240	
ACC AAC GGT GTT CTT OCT GTT GAT GCA OCT GTT GAT GCA GCT GGT GCA	768
Thr Asn Gly Val Leu Ala Val Asp Ala Ala Val Val Ala Ala Gly Ala	
245 250 255	
CAC TCC AAG TCT CTT OCT AAC TCC CTT GGT GAT GAC ATC CCA TTG GAT	816
His Ser Lys Ser Leu Ala Asn Ser Leu Gly Asp Asp Ile Pro Leu Asp	
260 265 270	
ACC GAA CGT GGA TAC CAC ATC GTG ATC GCC AAC CCA GAA GCT GCT CCA	864
Thr Glu Arg Gly Tyr His Ile Val Ile Ala Asn Pro Glu Ala Ala Pro	
275 280 285	
CCT ATT CCA ACT ACC GAT GCT TCT GGA AAG TTC ATC GCT ACT CCT ATG	912

095612400400

-continued

Arg Ile Pro Thr Thr Asp Ala Ser Gly Lys Phe Ile Ala Thr Pro Met	290	295	300	
GAG ATG GGT CTT CGT GTT GCT GGA ACC GTT GAG TTC GCT GGT CTC ACT	305	310	315	960
Glu Met Gly Leu Arg Val Ala Gly Thr Val Glu Phe Ala Gly Leu Thr				320
GCT GCT CCT AAC TGG AAG CGT GCT CAC GTT CTC TAC ACT CGC GCT CGT	325	330		1008
Ala Ala Pro Asn Trp Lys Arg Ala His Val Leu Tyr Thr Arg Ala Arg				335
AAG TTG CTT CCA GCT CTC GCT CCT GCC AGT TCT GAA GAA CGT TAC TCC	340	345		1056
Lys Leu Leu Pro Ala Leu Ala Pro Ala Ser Ser Glu Glu Arg Tyr Ser				
AAG TGG ATG GGT TTC CGT CCA AGC ATC CCG GAT TCC CTT CCA GTG ATT	355	360	365	1104
Lys Trp Met Gly Phe Arg Pro Ser Ile Pro Asp Ser Leu Pro Val Ile				
GCT CGT OCT ACC COT ACT CCA GAC GTT ATC TAC GCT TTC OGT CAC GGT	370	375	380	1152
Gly Arg Ala Thr Arg Thr Pro Asp Val Ile Tyr Ala Phe Gly His Gly				
CAC CTC GGT ATG ACT GGT GCT CCA ATG ACC GCA ACC CTC GTT TCT GAG	385	390	395	1200
His Leu Gly Met Thr Gly Ala Pro Met Thr Ala Thr Leu Val Ser Glu				400
CTC CTC GCA GGT GAG AAG ACC TCT ATC GAC ATC TCT CCA TTC GCA CCA	405	410		1248
Leu Leu Ala Gly Glu Lys Thr Ser Ile Asp Ile Ser Pro Phe Ala Pro				
AAC CGT TTC GGT ATT OGT AAG TCC AAG CAA ACT GGT CCT GCA TCC TAA	420	425	430	1296
Asn Arg Phe Gly Ile Gly Lys Ser Lys Glu Thr Gly Pro Ala Ser				

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Ala Glu Asn His Lys Lys Val Gly Ile Ala Gly Ala Gly Ile Val	1	5	10	15
Gly Val Cys Thr Ala Leu Met Leu Glu Arg Arg Gly Phe Lys Val Thr	20	25		30
Leu Ile Asp Pro Asn Pro Pro Gly Glu Gly Ala Ser Phe Gly Asn Ala	35	40	45	
Gly Cys Phe Asn Gly Ser Ser Val Val Pro Met Ser Met Pro Gly Asn	50	55	60	
Leu Thr Ser Val Pro Lys Trp Leu Leu Asp Pro Met Gly Pro Leu Ser	65	70	75	80
Ile Arg Phe Gly Tyr Phe Pro Thr Ile Met Pro Trp Leu Ile Arg Phe	85		90	95
Leu Leu Ala Gly Arg Pro Asn Lys Val Lys Glu Glu Ala Lys Ala Leu	100	105		110
Arg Asn Leu Ile Lys Ser Thr Val Pro Leu Ile Lys Ser Leu Ala Glu	115	120	125	
Glu Ala Asp Ala Ser His Leu Ile Arg His Glu Gly His Leu Thr Val	130	135	140	
Tyr Arg Gly Glu Ala Asp Phe Ala Arg Asp Arg Gly Gly Trp Glu Leu	145	150	155	160
Arg Arg Leu Asn Gly Val Arg Thr Glu Ile Leu Ser Ala Asp Ala Leu	165	170	175	

5,776,760

65

66

-continued

Arg	Asp	Phe	Asp	Pro	Asn	Leu	Ser	His	Ala	Phe	Thr	Lys	Gly	Ile	Leu	
180								185				190				
Ile	Glu	Glu	Asn	Gly	His	Thr	Ile	Asn	Pro	Gly	Gly	Leu	Val	Thr	Leu	
195							200				205					
Leu	Phe	Arg	Arg	Phe	Ile	Ala	Asn	Gly	Gly	Gly	Glu	Phe	Val	Ser	Ala	Arg
210					215						220					
Val	Ile	Gly	Phe	Glu	Thr	Gly	Gly	Arg	Ala	Leu	Lys	Gly	Ile	Thr	Thr	
225				230					235				240			
Thr	Asn	Gly	Val	Leu	Ala	Val	Asp	Ala	Ala	Val	Val	Ala	Ala	Gly	Ala	
245							250					255				
His	Ser	Lys	Ser	Leu	Ala	Asn	Ser	Leu	Gly	Asp	Asp	Ile	Pro	Leu	Asp	
260							265				270					
Thr	Glu	Arg	Gly	Tyr	His	Ile	Val	Ile	Ala	Asn	Pro	Glu	Ala	Ala	Pro	
275						280					285					
Arg	Ile	Pro	Thr	Thr	Asp	Ala	Ser	Gly	Lys	Phe	Ile	Ala	Thr	Pro	Met	
290					295					300						
Glu	Met	Gly	Leu	Arg	Val	Ala	Gly	Thr	Val	Glu	Phe	Ala	Gly	Leu	Thr	
305					310				315				320			
Ala	Ala	Pro	Asn	Trp	Lys	Arg	Ala	His	Val	Leu	Tyr	Thr	Arg	Ala	Arg	
325							330					335				
Lys	Leu	Leu	Pro	Ala	Leu	Ala	Pro	Ala	Ser	Ser	Glu	Glu	Arg	Tyr	Ser	
340							345					350				
Lys	Trp	Met	Gly	Phe	Arg	Pro	Ser	Ile	Pro	Asp	Ser	Leu	Pro	Val	Ile	
355						360					365					
Gly	Arg	Ala	Thr	Arg	Thr	Pro	Asp	Val	Ile	Tyr	Ala	Phe	Gly	His	Gly	
370						375					380					
His	Leu	Gly	Met	Thr	Gly	Ala	Pro	Met	Thr	Ala	Thr	Leu	Val	Ser	Glu	
385					390					395				400		
Leu	Leu	Ala	Gly	Glu	Lys	Thr	Ser	Ile	Asp	Ile	Ser	Pro	Phe	Ala	Pro	
405							410					415				
Asn	Arg	Phe	Gly	Ile	Gly	Lys	Ser	Lys	Gly	Thr	Gly	Pro	Ala	Ser		
420						425						430				

(2) INFORMATION FOR SBQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SBQ ID NO:19:

CGTTCTCTAC ACTCGTGCTC GTAAAGTTGC

29

(2) INFORMATION FOR SBQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SBQ ID NO:20:

CGTTCTCTAC ACTAAGGCTC GTAAAGTTGC

29

(2) INFORMATION FOR SBQ ID NO:21:

-continued

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGTTCTCTAC ACTCAAGCTC GTAAGTTGC

2 9

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGTTCTCTAC ACTGCTGCTC GTAAGTTGC

2 9

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTCTACACTT GGGCTCGTAA GCTTCTTCCA GC

3 2

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTCTACACTA TCGCTCGTAA GCTTCTTCCA GC

3 2

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CTCTACACTC TGGCTCGTAA GCTTCTTCCA GC

3 2

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

-continued

(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTCTACACTG AAGCTCGTAA GCTTCTTCCA GC

3 2

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CGCTGGAGCT GGAATCGTTG GTGTATGCAC TGCTTGATG CTTCAACGTC GTGGATTCAA

6 0

AG

6 2

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCAGATCCTC TCTGCTGATG CTTTGCCTGA TTTCGATCCT AACTTGTC TC ATGCTTTAC

6 0

CAAGG

6 5

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTCATCGGT T TGAGACTGA AAGTCGTCT CTCAAAGGCA T

4 1

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TACAACCACT AACGCGTCTTC TGGCTGTTGA TGCAGCTGTT GTTGCAAGCTG GTGCACACTC

6 0

TAAATCACT

6 9

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid

5,776,760

71

72

-continued

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GGAAATGGGT CTTCGTGTG CTGGTACTGT TGAGTTGCT GGTCTCACAG CTGCTCCTAA 60

C

61

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGGATGGTT TTCGTCTAG CATTCTGAT TCTCTTCCAG TGATGGTCG TGCAACTCGT 60

ACACCCGA

68

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGTAATCTAT OCTTTGGTC ACGGTCACT CGGTATGACA GGTGCTCCAA TGACTGCAAC 60

TCTCCTCTC

69

096124004 - 00200000